

the production of fertile pollen.

Sequence 5620 BP; 1498 A; 1360 C; 1328 G; 1430 T; 4 other;

Query Match 93.7%; Score 320.4; DB 13; Length 5620;

Best Local Similarity 98.0%; Pred. No. 5.2e-102;

Matches 333; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

1 atgttaccggtttatcaacacgtttgacgggttgctggtatcttcacacatacaaa 60

1138 atgttaccggtttatcaacacgtttgacgggttgctggtatcttcacacatacaaa 1080

61 gctaccggtatcaacacgtttgacgggttgctggtatcttcacacatacaaa 120

1079 gctaccggtatcaacacgtttgacgggttgctggtatcttcacacatacaaa 1020

121 aggttaccggtttatcaacacgtttgacgggttgctggtatcttcacacatacaaa 180

1019 aggttaccggtttatcaacacgtttgacgggttgctggtatcttcacacatacaaa 960

181 ggaagcgaacacgtttgacgggttgctggtatcttcacacatacaaa 240

959 ggaagcgaacacgtttgacgggttgctggtatcttcacacatacaaa 900

241 atcaggttcaagaacacgtttgacgggttgctggtatcttcacacatacaaa 300

899 atcaggttcaagaacacgtttgacgggttgctggtatcttcacacatacaaa 840

301 aacgagcattatcaacacgtttgacgggttgctggtatcttcacacatacaaa 342

839 aacgagcattatcaacacgtttgacgggttgctggtatcttcacacatacaaa 798

RESULT 14

AAV60972 standard; DNA; 344 BP.

AAV60972; (first entry)

03-DEC-1998 (first entry)

Barnase coding sequence.

Barnase: barnase; IPGR; Inverse polymerase chain reaction; phenotype: transgenic plant; hybrid seed; male sterile plant; active enzyme; regulatory protein; embryoleth seed; herbicide resistance; ss.

Synthetic.

Key Location/Qualifiers

CDS 9..344

27-AUG-1998. /product= "barnase"

20-FEB-1998; 98MC-GB00542.

21-FEB-1997; 97GB-0003681.

(GENE-) GENE SHEARS PTY LTD.

Betzner AS, Hultner E, Paul W, Perez P;

WPI; 1998-467572/40.

P-PSDB; AAW71703.

Production of transgenic plants having a desired phenotype - by using a pair of parent plants which each produce a polypeptide which complement each other when crossed

Example 1; Fig 1A; 58pp; English.

The present invention describes a pair of parent plants for producing seeds comprising: (a) a first parent plant containing at least 1 gene sequence encoding a polypeptide or protein A, and (b) a second parent plant containing at least 1 gene sequence encoding a polypeptide or protein B, where the polypeptides A and B, when expressed in separate plants, do not form an active enzyme, a regulatory protein or protein which affects the functionality and/or viability and/or the structural integrity of a cell, but when expressed in the same plant do form an active enzyme, regulatory protein, or protein which affects the structural integrity of a cell. Also described is a method for producing a plant having a desired phenotype by virtue of an active enzyme, a regulatory protein or a protein which affects the structural integrity of a cell comprising crossing a first line with a second line where the first line contains one or more gene sequences encoding a polypeptide or protein A but which line does not have the desired phenotype and where the second line contains one or more gene sequences encoding a polypeptide or protein B which is complementary to the polypeptide or protein A but which line does not have the desired phenotype. The method can be used for producing plants having altered phenotypes, e.g. male-sterility, embryoleth seeds, altered biochemical (e.g. fatty acid) composition or herbicide resistance. The present sequence encodes barnase which is used in an example from the present invention.

Sequence 344 BP; 114 A; 80 C; 78 G; 72 T; 0 other;

Query Match 93.5%; Score 319.6; DB 19; Length 344;

Best Local Similarity 98.8%; Pred. No. 2.4e-102;

Matches 322; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

8 cgttattcaacacgtttgacgggttgctggtatcttcacacatacaaaactct 67

15 cagttattcaacacgtttgacgggttgctggtatcttcacacatacaaaactct 74

68 gataattcaacacgtttgacgggttgctggtatcttcacacatacaaaactct 127

75 gataattcaacacgtttgacgggttgctggtatcttcacacatacaaaactct 134

128 cttagagacgttcgctcggaagacatcggtggaacatcttcacacatacaaaactct 187

133 cttagagacgttcgctcggaagacatcggtggaacatcttcacacatacaaaactct 194

188 aaactccgggcaaaagcgagacatcggtggaacatcttcacacatacaaaactct 247

195 aaactccgggcaaaagcgagacatcggtggaacatcttcacacatacaaaactct 254

248 tttagaattcaacacgtttgacgggttgctggtatcttcacacatacaaaactct 307

255 tttagaattcaacacgtttgacgggttgctggtatcttcacacatacaaaactct 314

308 cattatcagacattcaaaactcag 333

315 cattatcagacattcaaaactcag 340

RESULT 15

AAQ27104 standard; DNA; 791 BP.

AAQ27104; (first entry)

26-JAN-1993

BN ribonuclease.

Barnase; calcium; Tyl; M13; pGN1330; BN ORF; retrotransposon; replication; ss.

Bacillus amyloliquefaciens.

XX

PS

XX

Db 2565 GCTACCTGATTAATTCATTCATCAAAATCAAGCAAAAGCCCTGCGCTGGGATCAACAA 2506  
 QY 121 agggaaacctgacagcgtcgtccgggaaagacatcgycgagacatctctcaaacag 180  
 Db 2505 AGGGAACCTTGCAACACCTCCTCCGGGAAAGCATGCGCGGACATCTCTCAAAACAG 2446  
 QY 181 ggaaggaacactcccgagcaaaagcgagacacatcgycgtgaagcgagatataac 240  
 Db 2445 GGAAGCAAACTCCCGGCAAAAGCGAGCAATGCGGTGAAGCGGATATTAATATAC 2386  
 QY 241 atcagcttcagaaatcagacgagatcttactcaagcgactgctgatttacaacaa 300  
 Db 2385 ATCAGCTTCAGAAATTCACACCGGATCTTACTCAAGGACTGGCTGATTTCAAAAC 2326  
 QY 301 aacggacattatcagacaccttcaaaaataag 333  
 Db 2325 AACGACATTATTCAGACCTTACAAAATCAG 2293  
 IS-08-894-440-4/C  
 Sequence 7 Application US/08894440  
 Patent No. 6025346  
 Applicant: PLANT GENETIC SYSTEMS N.V.  
 Title of Invention: Method to obtain male sterile plants  
 File Reference: NMSCOR  
 Current Application Number: US/08/894,440  
 Current Filing Date: 1997-11-12  
 Number of Seq ID Nos: 4  
 Software: Patent In Ver. 2.0  
 Seq ID No 4  
 Length: 5864  
 Type: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: T-DNA of  
 OTHER INFORMATION: plasmid pPCO13  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((1)..(23))  
 OTHER INFORMATION: Right border of Agrobacterium T-DNA (RB)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((98)..(330))  
 OTHER INFORMATION: region containing polyadenylation signal of gene 7  
 OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((331)..(882))  
 OTHER INFORMATION: region coding for phosphinothricin acetyl  
 OTHER INFORMATION: transferase (bar)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((883)..(2608))  
 OTHER INFORMATION: promoter of small subunit gene of Rubisco of  
 OTHER INFORMATION: Arabidopsis (Pasu)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((2659)..(3031))  
 OTHER INFORMATION: region containing polyadenylation signal of  
 OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA  
 OTHER INFORMATION: (3 nos)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((3032)..(3367))  
 OTHER INFORMATION: region coding for barnase of Bacillus  
 OTHER INFORMATION: amyloliquefaciens  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((3368)..(4877))  
 OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana

*Handwritten signature*

OTHER INFORMATION: tabacum (PTA29)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (4924)..(5216)  
 OTHER INFORMATION: promoter of nopaline synthase gene of  
 OTHER INFORMATION: Agrobacterium T-DNA (Pnos)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (5217)..(5489)  
 OTHER INFORMATION: region coding for barstar of Bacillus  
 OTHER INFORMATION: amyloliquefaciens  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (5490)..(5765)  
 OTHER INFORMATION: region containing polyadenylation signal of gene 7  
 OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((5840)..(5864))  
 OTHER INFORMATION: left border of Agrobacterium T-DNA  
 US-08-894-440-4

Query Match 93.7%; Score 320.4; DB 3; Length 5864;  
 Best Local Similarity 98.0%; Pred. No. 7.5e-102;  
 Matches 335; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 atggtacgggttatacaacagttgacgggttcgagatattcttcaagacatatacaaa 60  
 Db 3367 ATGGTACGGGTTA-TCAACAGTTTGACGGGCTTGCGGATTTCAAGCATATCATRA 3309  
 QY 61 gctaccgtaattacattacaaaatacagaagacagcctcgctgggtggatcaaa 120  
 Db 3308 GCTACCTGATTAATTCATTACAAAATCAGAACACAAACCTTCGCTGGGTGGATCAAA 3249  
 QY 121 agggaaaccttgacagcgtcgtccgggaaagacatcgycgtgaagcgagatatac 180  
 Db 3248 AGGGAACCTTGCAACAGTGTGCTCCGGGAAAGCATGCGGAGACATCTCTCAAAACG 3189  
 QY 181 ggaaggaacactcccgagcaaaagcgagacatcgycgtgaagcgagatatac 240  
 Db 3188 GGAAGGAACACTCCCGGCAAAAGCGAGCAACATGCGGTCAACCGGATTTAACTATAC 3129  
 QY 241 atcagcttcagaaatcagaccgagatcttactcaagcgactgctgatttacaacaa 300  
 Db 3128 ATCAGCTTCAGAAATTCAGACCGGATCTTACTCAAGCGACTGCTGATTTACAAAC 3069  
 QY 301 aacggacattatcagacaccttacaacaaatcagtaactaga 342  
 Db 3068 AACGACATTATTCAGACCTTACAAAATCAGATACGAAA 3027

Search completed: September 7, 2001, 14:47:02  
 Job time: 48 sec

*deleted in QY*